PCS10350APME

SEQUENCE LISTINGS

5   SEQ ID NO. 1

SEQ ID No. 1 is the amino acid sequence for HSPDE1B2. For comparative purposes the sequence for HSPDE1B1 is shown in as a comparison using CLUSTAL W (1.74) multiple sequence alignment

```
HSPDE1B1    MELSPRSPPEMLEESDCPSPLELKSAPSKKMWIKLRSLLRYMVKQLENGEINIEELKKNL
HSPDE1B2    ---------------MANPVPVQRSHLQGPILRLR----YMVKQLENGEINIEELKKNL
            ..*: :: : :    ::**   ******************

HSPDE1B1    EYTASLLEAVYIDETRQILDTEDELQELRSDAVPSEVRDWLASTFTQQARAKGRRAEEKP
HSPDE1B2    EYTASLLEAVYIDETRQILDTEDELQELRSDAVPSEVRDWLASTFTQQARAKGRRAEEKP
            ***********************************************************

HSPDE1B1    KFRSIVHAVQAGIFVERMFRRTYTSVGPTYSTAVLNCLKNLDLWCFDVFSLNQAADDHAL
HSPDE1B2    KFRSIVHAVQAGIFVERMFRRTYTSVGPTYSTAVLNCLKNLDLWCFDVFSLNQAADDHAL
            ***********************************************************

HSPDE1B1    RTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKYKNPYHNQIHAADVTQTVHCFLL
HSPDE1B2    RTIVFELLTRNNLISRFKIPTVFLMSFLDALETGYGKYKNPYHNQIHAADVTQTVHCFLL
            **********:************************************************

HSPDE1B1    RTGMVHCLSEIELLAIIFAAAIHDYEHTGTTNSFHIQTKSECAIVYNDRSVLENHHISSV
HSPDE1B2    RTGMVHCLSEIELLAIIFAAAIHDYEHTGTTNSFHIQTKSECAIVYNDRSVLENHHISSV
            ***********************************************************

HSPDE1B1    FRLMQDDEMNIFINLTKDEFVELRALVIEMVLATDMSCHFQQVKTMKTALQQLERIDKPK
HSPDE1B2    FRLMQDDEMNIFINLTKDEFVELRALVIEMVLATDMSCHFQQVKTMKTALQQLERIDKPK
            ***********************************************************

HSPDE1B1    ALSLLLHAADISHPTKQWLVHSRWTKALMEEFFRQGDKEAELGLPFSPLCDRTSTLVAQS
HSPDE1B2    ALSLLLHAADISHPTKQWLVHSRWTKALMEEFFRQGDKEAELGLPFSPLCDRTSTLVAQS
            ***********************************************************

HSPDE1B1    QIGFIDFIVEPTFSVLTDVAEKSVQPLADEDSKSKNQPSFQWRQPSLDVEVGDPNPDVVS
HSPDE1B2    QIGFIDFIVEPTFSVLTDVAEKSVQPLADEDSKSKNQPSFQWRQPSLDVEVGDPNPDVVS
            ***********************************************************

HSPDE1B1    FRSTWVKRIQENKQKWKERAASGITNQMSIDELSPCEEEAPPSPAEDEHNQNGNLD
HSPDE1B2    FRSTWVKRIQENKQKWKERAASGITNQMSIDELSPCEEEAPPSPAEDEHNQNGNLD
            *******************************************************
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SEQ ID NO. 2

SEQ ID No. 2 is the nucleotide sequence for HSPDE1B2. For comparative purposes the sequence for HSPDE1B1 is shown in as a comparison using CLUSTAL W (1.74) multiple sequence alignment

```
HSPDE1B1    GTCGACCCACGCGTCCGCCCACGCGTCCGGCCTAGAGACACCGGCCTGGCTGGTCCACGC
HSPDE1B2    GTCGACCCACGCGTCCGGG-AGGAGGAAGGC--AGGGGCCAAAGAGGAAGTTGTCCCCTC
            ****************** * * * *** ** * *   *    * **** * *

HSPDE1B1    CAGCCGCAGACCGTGGCTGAGCATGGAGCTGTCCCCCCGCAGTCCTCCGGAGATGCTGGA
HSPDE1B2    TTGGGGG---CCCTGGG-GCTCCTGGGG-T--C--AGGATTTTGATACTCTGAAGCAGGA
             *  *   ** *** *  * *** * *  *     * *  ** ** ***

HSPDE1B1    GGAGTCGGATTGCCC--GTCACCCCTGGAGCTGAAGTCAGCCCCCAGCAAGAAGATGTGG
HSPDE1B2    A-ACTTTGATTCCCATGGCAAACCCTGTTCCTGTTCAGAGGAGCCACCTCCAGG------
             * *  **** **   *  * ***** ***    **   *** *    * *

HSPDE1B1    ATTAAGCTTCGGTCTCTG-CTGCGCTACATGGTGAAGCAGTTGGAGAATGGGGAGATAAA
HSPDE1B2    -----GCCCCATTCTCAGGCTGCGCTACATGGTGAAGCAGTTGGAGAATGGGGAGATAAA
                 ** * **** * ********************************************

HSPDE1B1    CATTGAGGAGCTGAAGAAAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGTCTACAT
HSPDE1B2    CATTGAGGAGCTGAAGAAAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGTCTACAT
            ************************************************************

HSPDE1B1    AGATGAGACACGGCAAATCTTGGACACGGAGGACGAGCTGCAGGAGCTGCGGTCAGATGC
HSPDE1B2    AGATGAGACACGGCAAATCTTGGACACGGAGGACGAGCTGCAGGAGCTGCGGTCAGATGC
            ************************************************************

HSPDE1B1    CGTGCCTTCGGAGGTGCGGGACTGGCTGGCCTCCACCTTCACCCAGCAGGCCCGGGCCAA
HSPDE1B2    CGTGCCTTCGGAGGTGCGGGACTGGCTGGCCTCCACCTTCACCCAGCAGGCCCGGGCCAA
            ************************************************************

HSPDE1B1    AGGCCGCCGAGCAGAGGAGAAGCCCAAGTTCCGAAGCATTGTGCACGCTGTGCAGGCTGG
HSPDE1B2    AGGCCGCCGAGCAGAGGAGAAGCCCAAGTTCCGAAGCATTGTGCACGCTGTGCAGGCTGG
            ************************************************************

HSPDE1B1    GATCTTCGTGGAACGGATGTTCCGGAGAACATACACCTCTGTGGGCCCCACTTACTCTAC
HSPDE1B2    GATCTTCGTGGAACGGATGTTCCGGAGAACATACACCTCTGTGGGCCCCACTTACTCTAC
            ************************************************************

HSPDE1B1    TGCGGTTCTCAACTGTCTCAAGAACCTGGATCTCTGGTGCTTTGATGTCTTTTCCTTGAA
HSPDE1B2    TGCGGTTCTCAACTGTCTCAAGAACCTGGATCTCTGGTGCTTTGATGTCTTTTCCTTGAA
            ************************************************************

HSPDE1B1    CCAGGCAGCAGATGACCATGCCCTGAGGACCATTGTTTTTGAGTTGCTGACTCGGCATAA
HSPDE1B2    CCAGGCAGCAGATGACCATGCCCTGAGGACCATTGTTTTTGAGTTGCTGACTCGGCATAA
            ************************************************************

HSPDE1B1    CCTCATCAGCCGCTTCAAGATTCCCACTGTGTTTTTGATGAGTTTCCTGGATGCCTTGGA
HSPDE1B2    CCTCATCAGCCGCTTCAAGATTCCCACTGTGTTTTTGATGAGTTTCCTGGATGCCTTGGA
            ************************************************************

HSPDE1B1    GACAGGCTATGGGAAGTACAAGAATCCTTACCACAACCAGATCCACGCAGCCGATGTTAC
HSPDE1B2    GACAGGCTATGGGAAGTACAAGAATCCTTACCACAACCAGATCCACGCAGCCGATGTTAC
            ************************************************************

HSPDE1B1    CCAGACAGTCCATTGCTTCTTGCTCCGCACAGGGATGGTGCACTGCCTGTCGGAGATTGA
HSPDE1B2    CCAGACAGTCCATTGCTTCTTGCTCCGCACAGGGATGGTGCACTGCCTGTCGGAGATTGA
            ************************************************************

HSPDE1B1    GCTCCTGGCCATCATCTTTGCTGCAGCTATCCATGATTATGAGCACACGGGCACTACCAA
HSPDE1B2    GCTCCTGGCCATCATCTTTGCTGCAGCTATCCATGATTATGAGCACACGGGCACTACCAA
            ************************************************************

HSPDE1B1    CAGCTTCCACATCCAGACCAAGTCAGAATGTGCCATCGTGTACAATGATCGTTCAGTGCT
HSPDE1B2    CAGCTTCCACATCCAGACCAAGTCAGAATGTGCCATCGTGTACAATGATCGTTCAGTGCT
            ************************************************************

HSPDE1B1    GGAGAATCACCACATCAGCTCTGTTTTCCGATTGATGCAGGATGATGAGATGAACATTTT
HSPDE1B2    GGAGAATCACCACATCAGCTCTGTTTTCCGATTGATGCAGGATGATGAGATGAACATTTT
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        HSPDE1B1    CATCAACCTCACCAAGGATGAGTTTGTAGAACTCCGAGCCCTGGTCATTGAGATGGTGTT
        HSPDE1B2    CATCAACCTCACCAAGGATGAGTTTGTAGAACTCCGAGCCCTGGTCATTGAGATGGTGTT
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        HSPDE1B1    GGCCACAGACATGTCCTGCCATTTCCAGCAAGTGAAGACCATGAAGACAGCCTTGCAACA
        HSPDE1B2    GGCCACAGACATGTCCTGCCATTTCCAGCAAGTGAAGACCATGAAGACAGCCTTGCAACA
                    ************************************************************

 10     HSPDE1B1    GCTGGAGAGGATTGACAAGCCCAAGGCCCTGTCTCTACTGCTCCATGCTGCTGACATCAG
        HSPDE1B2    GCTGGAGAGGATTGACAAGCCCAAGGCCCTGTCTCTACTGCTCCATGCTGCTGACATCAG
                    ************************************************************

 15     HSPDE1B1    CCACCCAACCAAGCAGTGGTTGGTCCACAGCCGTTGGACCAAGGCCCTCATGGAGGAATT
        HSPDE1B2    CCACCCAACCAAGCAGTGGTTGGTCCACAGCCGTTGGACCAAGGCCCTCATGGAGGAATT
                    ************************************************************

        HSPDE1B1    CTTCCGTCAGGGTGACAAGGAGGCAGAGTTGGGCCTGCCCTTTTCTCCACTCTGTGACCG
        HSPDE1B2    CTTCCGTCAGGGTGACAAGGAGGCAGAGTTGGGCCTGCCCTTTTCTCCACTCTGTGACCG
 20                 ************************************************************

        HSPDE1B1    CACTTCCACTCTAGTGGCACAGTCTCAGATAGGGTTCATCGACTTCATTGTGGAGCCCAC
        HSPDE1B2    CACTTCCACTCTAGTGGCACAGTCTCAGATAGGGTTCATCGACTTCATTGTGGAGCCCAC
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        HSPDE1B1    ATTCTCTGTGCTGACTGACGTGGCAGAGAAGAGTGTTCAGCCCCTGGCGGATGAGGACTC
        HSPDE1B2    ATTCTCTGTGCTGACTGACGTGGCAGAGAAGAGTGTTCAGCCCCTGGCGGATGAGGACTC
                    ************************************************************

 30     HSPDE1B1    CAAGTCTAAAAACCAGCCCAGCTTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGG
        HSPDE1B2    CAAGTCTAAAAACCAGCCCAGCTTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGG
                    ************************************************************

 35     HSPDE1B1    AGACCCCAACCCTGATGTGGTCAGCTTTCGTTCCACCTGGGTCAAGCGCATTCAGGAGAA
        HSPDE1B2    AGACCCCAACCCTGATGTGGTCAGCTTTCGTTCCACCTGGGTCAAGCGCATTCAGGAGAA
                    ************************************************************

        HSPDE1B1    CAAGCAGAAATGGAAGGAACGGGCAGCAAGTGGCATCACCAACCAGATGTCCATTGACGA
        HSPDE1B2    TAAGCAGAAATGGAAGGAACGGGCAGCAAGTGGCATCACCAACCAGATGTCCATTGACGA
 40                  ***********************************************************

        HSPDE1B1    GCTGTCCCCCTGTGAAGAAGAGGCCCCCCCCATCCCCTGCCGAAGATGAACACAACCAGAA
        HSPDE1B2    GCTGTCCCCCTGTGAAGAAGAGGCCCCCCCCATCCCCTGCCGAAGATGAACACAACCAGAA
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        HSPDE1B1    TGGGAATCTGGATTAGCCCTGGGGCTGGCCCAGGTCTTCATTGAGTCCAAAGTGTTTGAT
        HSPDE1B2    TGGGAATCTGGATTAGCCCTGGGGCTGGCCCAGGTCTTCATTGAGTCCAAAGTGTTTGAT
                    ************************************************************

 50     HSPDE1B1    GTCATCAGCACCATCCATCAGGACTGGCTCCCCCATCTGCTCCAAGGGAGCGTGGTCGTG
        HSPDE1B2    GTCATCAGCACCATCCATCAGGACTGGCTCCCCCATCTGCTCCAAGGGAGCGTGGTCGTG
                    ************************************************************

 55     HSPDE1B1    GAAGAAACAACCCACCTGAAGGCCAAATGCCAGAGATTTGGGGTTGGGGAAAGGGCCCCT
        HSPDE1B2    GAAGAAACAACCCACCTGAAGGCCAAATGCCAGAGATTTGGGGTTGGGGAAAGGGCCCCT
                    ************************************************************

        HSPDE1B1    CCCCACCTGACACCCACTGGGGTGCACTTTAATGTTCCGGCAGCAAGACTGGGGAACTTC
        HSPDE1B2    CCCCACCTGACACCCACTGGGGTGCACTTTAATGTTCCGGCAGCAAGACTGGGGAACTTC
 60                 ************************************************************

        HSPDE1B1    AGGCTCCCAGTGGTCACTGTGCCCATCCCTCAGCCTCTGGATTCTCTTCATGGCCAGGTG
        HSPDE1B2    AGGCTCCCAGTGGTCACTGTGCCCATCCCTCAGCCTCTGGATTCTCTTCATGGCCAGGTG
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        HSPDE1B1    GCTGCCAGGGAGCGGGGAGCTTCCTGGAGGCTTCCCAGGGCCTTGGGGAAGGGTCAGAGA
        HSPDE1B2    GCTGCCAGGGAGCGGGGAGCTTCCTGGAGGCTTCCCAGGGCCTTGGGGAAGGGTCAGAGA
                    ************************************************************

 70     HSPDE1B1    TGCCAGCCCCCTGGGACCTCCCCCATCCTTTTTGCCTCCAAGTTTCTAAGCAATACATTT
        HSPDE1B2    TGCCAGCCCCCTGGGACCTCCCCCATCCTTTTTGCCTCCAAGTTTCTAAGCAATACATTT
                    ************************************************************

        HSPDE1B1    TGGGGGTTCCCTCAGCCCCCCACCCCAGATCTTAGCTGGCAGGTCTGGGTGCCCCTTTTC
 75     HSPDE1B2    TGGGGGTTCCCTCAGCCCCCCACCCCAGATCTTAGCTGGCAGGTCTGGGTGCCCCTTTTC
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HSPDE1B1   CTCCCCTGGGAAGGGCTGGAATAGGATAGAAAGCTGGGGGTTTTCAGAGCCCTATGTGTG
HSPDE1B2   CTCCCCTGGGAAGGGCTGGAATAGGATAGAAAGCTGGGGGTTTTCAGAGCCCTATGTGTG
           ************************************************************
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HSPDE1B1   GGGAGGGGAGTGGATTCCTTCAGGGCATGGTACCTTTCTAGGACCTGGGAATGGGGTGGA
HSPDE1B2   GGGAGGGGAGTGGATTCCTTCAGGGCATGGTACCTTTCTAGGATCTGGGAATGGGGTGGA
           ******************************************** ***************
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HSPDE1B1   GAGGACATCCTCTTCACCCCAGAATTGCGCTGCTTCAGCCCCATCTCCAGCCTGATCCTC
HSPDE1B2   GAGGACATCCTCTTCACCCCAGAATTGCGCTGCTTCAGCCCCATCTCCAGCCTGATCCTC
           ************************************************************
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15
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HSPDE1B1   TGAATCTTCCTTCCCTCCCTTTCTGATATAGTGACTGGGGCAAAAGGAGCCATTGTGACC
HSPDE1B2   TGAATCTTCCTTCCCTCCCTTTCTGATACAGTGACTGGGGCAAAAGGAGCCATTGTGACC
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20
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HSPDE1B1   AGGGGCTGCGGGAGGCCTTTCCTGGGACCTTCCTTGGGACTGGTCTGGGCCCCTGGGGCT
HSPDE1B2   AGGGGCTGCGGGAGGCCTTTCCTGGGACCTTCCTTGGGACTGGTCTGGGCCCCTGGGGCT
           ************************************************************
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25
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HSPDE1B1   TGTCGCCTGCCCTGAGTCCGGAGCCCTTTGCCTCCTTCCTCTCCCCTGGGGCTGGGAGGC
HSPDE1B2   TGTCGCCTGCCCTGAGTCCGGAGCCCTTTGCCTCCTTCCTCTCCCCTGGGGCTGGGAGGC
           ************************************************************
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30
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HSPDE1B1   TCCATCCGACCAATGTCTGTAAAGTGCTTTGAGGATCTCCCCAGCAAAGCACCTTCAGAA
HSPDE1B2   TCCATCCGACCAATGTCTGTAAAGTGCTTTGAGGATCTCCCCAGCAAAGCACCTTCAGAA
           ************************************************************
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35
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HSPDE1B1   TGTATCGACACCAGCTGGGTTAGGGTCAAGGGTGCCTGGGGAGGGTGAGTAATCCTGCAT
HSPDE1B2   TGTATCGACACCAGCTGGGTTAGGGTCAAGGGTGCCTGGGGAGGGTGAGTAATCCTGCAT
           ************************************************************
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HSPDE1B1   TGCTAAAAGAGAGGGTCTGTCCCCTCCTCTCCACGTCCCAGAACTGGCCCAGCTGCAGGC
HSPDE1B2   TGCTAAAAGAGAGGGTCTGTCCCCTCCTCTCCACGTCCCAGAACTGGCCCAGCTGCAGGC
           ************************************************************
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40
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HSPDE1B1   ACTAAGAAGCTCCTCCCCTGAGACAAGTGAGGGGTAGTCGGTGAAAGGCAGATGGACAAG
HSPDE1B2   ACTAAGAAGCTCCTCCCCTGAGACAAGTGAGGGGTAGTCGGTGAAAGGCAGATGGACAAG
           ************************************************************
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HSPDE1B1   GGGCTCAGGGCTGCTGCCTTCCTGTCCTCTGGAGAGAACCCAGCCAGGCGCGGTGCCCCT
HSPDE1B2   GGGCTCAGGGCTGCTGCCTTCCTGTCCTCTGGAGAGAACCCAGCCAGGCGCGGTGCCCCT
           ************************************************************
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HSPDE1B1   TCCTCTCCTCAGGCTCCTCCTTGCCCCCACCTTGCCCCAGGAAAGGCCAAAGTCCAGGTG
HSPDE1B2   TCCTCTCCTCAGGCTCCTCCTTGCCCCCACCTTGCCCCAGGAAAGGCCAAAGTCCAGGTG
           ************************************************************
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HSPDE1B1   ACTGCCCTCCTTCTTTCTTGTAAATACCAACCGTGCATTTGTACAGTGGGCCCTGTTCAT
HSPDE1B2   ACTGCCCTCCTTCTTTCTTGTAAATACCAACCATGCATTTGTACAGTGGGCCCTGTTCAT
           ******************************** ***************************
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55
```
HSPDE1B1   GCGAAATCCACATCCATGGTCTCCTAGACCTGCTACCCTGGTACTTCCACCCTACCCCAC
HSPDE1B2   GCGAAATCCACATCCATGGTCTCCTAGACCTGCTACCCTGGTACTTCCACCCTACCCCAC
           ************************************************************
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HSPDE1B1   CCCGAGAAGGGCAGAGACGCATGTGACTCACCCCTGCCCTTGGTTTCCCAGACCCCTGCT
HSPDE1B2   CCCGAGAAGGGCAGAGACGCATGTGACTCACCCCTGCCCTTGGTTTCCCAGACCCCTGCT
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HSPDE1B1   ACAGCCAGAGAACAATAAAGAAGGGAGACCAGGAAAAAAAAAAAAAAAAAAAAAAA
HSPDE1B2   ATAGCCAGAGAACAATAAAGAAGGGAGACCAGGAAAAAAAAAAAAAAAAAAAAAAAAA
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                ---------------MANPVPVQRSHLQGPILRLR----YMVKQLENGEINIEELKKNL
EYTASLLEAVYIDETRQILDTEDELQELRSDAVPSEVRDWLASTFTQQARAKGRRAEEKP
KFRSIVHAVQAGIFVERMFRRTYTSVGPTYSTAVLNCLKNLDLWCFDVFSLNQAADDHAL
RTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKYKNPYHNQIHAADVTQTVHCFLL
RTGMVHCLSEIELLAIIFAAAIHDYEHTGTTNSFHIQTKSECAIVYNDRSVLENHHISSV
FRLMQDDEMNIFINLTKDEFVELRALVIEMVLATDMSCHFQQVKTMKTALQQLERIDKPK
ALSLLLHAADISHPTKQWLVHSRWTKALMEEFFRQGDKEAELGLPFSPLCDRTSTLVAQS
QIGFIDFIVEPTFSVLTDVAEKSVQPLADEDSKSKNQPSFQWRQPSLDVEVGDPNPDVVS
FRSTWVKRIQENKQKWKERAASGITNQMSIDELSPCEEEAPPSPAEDEHNQNGNLD
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SEQ ID NO. 2

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GTCGACCCACGCGTCCGGG-AGGAGGAAGGC--AGGGGCCAAAGAGGAAGTTGTCCCCTC
TTGGGGG---CCCTGGG-GCTCCTGGGG-T--C--AGGATTTTGATACTCTGAAGCAGGA
A-ACTTTGATTCCCATGGCAAACCCTGTTCCTGTTCAGAGGAGCCACCTCCAGG------
GCCCCATTCTCAGGCTGCGCTACATGGTGAAGCAGTTGGAGAATGGGGAGATAAA
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CATTGAGGAGCTGAAGAAAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGTCTACAT
AGATGAGACACGGCAAATCTTGGACACGGAGGACGAGCTGCAGGAGCTGCGGTCAGATGC
CGTGCCTTCGGAGGTGCGGGACTGGCTGGCCTCCACCTTCACCCAGCAGGCCCGGGCCAA
AGGCCGCCGAGCAGAGGAGAAGCCCAAGTTCCGAAGCATTGTGCACGCTGTGCAGGCTGG
GATCTTCGTGGAACGGATGTTCCGGAGAACATACACCTCTGTGGGCCCCACTTACTCTAC
TGCGGTTCTCAACTGTCTCAAGAACCTGGATCTCTGGTGCTTTGATGTCTTTTCCTTGAA
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CCAGGCAGCAGATGACCATGCCCTGAGGACCATTGTTTTTGAGTTGCTGACTCGGCATAA
CCTCATCAGCCGCTTCAAGATTCCCACTGTGTTTTTGATGAGTTTCCTGGATGCCTTGGA
GACAGGCTATGGGAAGTACAAGAATCCTTACCACAACCAGATCCACGCAGCCGATGTTAC
CCAGACAGTCCATTGCTTCTTGCTCCGCACAGGGATGGTGCACTGCCTGTCGGAGATTGA
GCTCCTGGCCATCATCTTTGCTGCAGCTATCCATGATTATGAGCACACGGGCACTACCAA
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35

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CAGCTTCCACATCCAGACCAAGTCAGAATGTGCCATCGTGTACAATGATCGTTCAGTGCT
GGAGAATCACCACATCAGCTCTGTTTTCCGATTGATGCAGGATGATGAGATGAACATTTT
CATCAACCTCACCAAGGATGAGTTTGTAGAACTCCGAGCCCTGGTCATTGAGATGGTGTT
GGCCACAGACATGTCCTGCCATTTCCAGCAAGTGAAGACCATGAAGACAGCCTTGCAACA
GCTGGAGAGGATTGACAAGCCCAAGGCCCTGTCTCTACTGCTCCATGCTGCTGACATCAG
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CCACCCAACCAAGCAGTGGTTGGTCCACAGCCGTTGGACCAAGGCCCTCATGGAGGAATT
CTTCCGTCAGGGTGACAAGGAGGCAGAGTTGGGCCTGCCCTTTTCTCCACTCTGTGACCG
CACTTCCACTCTAGTGGCACAGTCTCAGATAGGGTTCATCGACTTCATTGTGGAGCCCAC
ATTCTCTGTGCTGACTGACGTGGCAGAGAAGAGTGTTCAGCCCCTGGCGGATGAGGACTC
CAAGTCTAAAAACCAGCCCAGCTTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGG
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AGACCCCAACCCTGATGTGGTCAGCTTTCGTTCCACCTGGGTCAAGCGCATTCAGGAGAA
TAAGCAGAAATGGAAGGAACGGGCAGCAAGTGGCATCACCAACCAGATGTCCATTGACGA
GCTGTCCCCCTGTGAAGAAGAGGCCCCCCCATCCCCTGCCGAAGATGAACACAACCAGAA
TGGGAATCCTGGATTAGCCCTGGGGCTGGCCCAGGTCTTCATTGAGTCCAAAGTGTTTGAT
GTCATCAGCACCATCCATCAGGACTGGCTCCCCCATCTGCTCCAAGGGAGCGTGGTCGTG
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GAAGAAACAACCCACCTGAAGGCCAAATGCCAGAGATTTGGGGTTGGGGAAAGGGCCCCT
CCCCACCTGACACCCACTGGGGTGCACTTTAATGTTCCGGCAGCAAGACTGGGGAACTTC
AGGCTCCCAGTGGTCACTGTGCCCATCCCTCAGCCTCTGAATTTCTCTTCATGGCCAGGTG
GCTGCCAGGGAGCGGGGAGCTTCCTGGAGGCTTCCAGGGCCTTGGGGAAGGGTCAGAGA
TGCCAGCCCCCTGGGACCTCCCCCATCCTTTTTGCCTCCAAGTTTCTAAGCAATACATTT
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TGGGGGTTCCCTCAGCCCCCCACCCCAGATCTTAGCTGGCAGGTCTGGGTGCCCCTTTTC
CTCCCCTGGGAAGGGCTGGAATAGGATAGAAAGCTGGGGGTTTTCAGAGCCCTATGTGTG
GGGAGGGGAGTGGATTCCTTCAGGGCATGGTACCTTTCTAGGATCTGGGAATGGGGTGGA
GAGGACATCCTCTTCACCCCAGAATTGCGCTGCTTCAGCCCCATCTCCAGCCTGATCCTC
TGAATCTTCCTTCCCTCCCTTTCTGATACAGTGACTGGGGCAAAAGGAGCCATTGTGACC
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AGGGGCTGCGGGAGGCCTTTCCTGGGACCTTCCTTGGGACTGGTCTGGGCCCCTGGGGCT
TGTCGCCTGCCCTGAGTCCGGAGCCCTTTGCCTCCTTCCTCTCCCCTGGGGCTGGGAGGC
TCCATCCGACCAATGTCTGTAAAGTGCTTTGAGGATCTCCCCAGCAAAGCACCTTCAGAA
TGTATCGACACCAGCTGGGTTAGGGTCAAGGGTGCCTGGGGAGGGTGAGTAATCCTGCAT
TGCTAAAAGAGAGGGTCTGTCCCCTCCTCTCCACGTCCCAGAACTGGCCCAGCTGCAGGC
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ACTAAGAAGCTCCTCCCCTGAGACAAGTGAGGGGTAGTCGGTGAAAGGCAGATGGACAAG
GGGCTCAGGGCTGCTGCCTTCCTGTCCTCTGGAGAGAACCCAGCCAGGCGCGGTGCCCCT
TCCTCTCCTCAGGCTCCTCCTTGCCCCCACCTTGCCCCAGGAAAGGCCAAAGTCCAGGTG
ACTGCCCTCCTTCTTTCTTGTAAATACCAACCATGCATTTGTACAGTGGGCCCTGTTCAT
GCGAAATCCACATCCATGGTCTCCTAGACCTGCTACCCTGGTACTTCCACCCTACCCCAC
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70

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CCCGAGAAGGGCAGAGACGCATGTGACTCACCCCTGCCCTTGGTTTCCCAGACCCCTGCT
ATAGCCAGAGAACAATAAAGAAGGGAGACCAGGAAAAAAAAAAAAAAAAAAAAAAA
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